```
===========================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: Tue Jun 19 17:34:09 EDT 2007
===========================================================
```

```
*********************************************************
Reviewer Comments:
<150>
<151>
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Please remove the above numeric identifiers, since no prior application
information is given.

```
<210> 3

 <211> 30

 <212> DNA

 <213> Artificial Sequence

        <220>

 <223> Description of Artificial Sequence:

     Oligonucleotide                        metAfw
```

Please move the "metAfw" over to the left, one space away from
"Oligonucleotide."

```
 <210> 6

 <211> 42     n=1:1:1:1 mixture of A,T,C and G.

 <212> DNA
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

GAPDHrevII

<400> 6

gaccttaatt aagatctcat atgttccacc agctatttgt ta   42

The <211> response shows invalid information: do not show explanatory
information on the <211> line; it belongs in the <220>-<223> section.
Also, no "n's" appear in the sequence. Same type of error in Sequences
10 and 12: no "n's" in those sequences, although an explanation
appears.

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide

metAmutfw1

<400> 9

nnncagatca cgccatacga tctac   25

The "n's" in the above sequence are not explained. Please explain them
in the <220>-<223> section. Same type of error in Sequence 11.

****

Application No: 10530843   Version No: 1.0

Input Set:

Output Set:

Started: 2007-06-19 16:47:51.252
Finished: 2007-06-19 16:47:52.739
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 487 ms
Total Warnings: 10
Total Errors: 10
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code	Error Description
E 201	Mandatory field data missing in <140>
E 201	Mandatory field data missing in <141>
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 202	Invalid input format; Value must be an integer in <211> in SEQ ID
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 253	The number of bases differs from <211> Input: 0 Calculated:42
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 342	'n' position not defined found at POS: 1 SEQID(9)
E 342	'n' position not defined found at POS: 2 SEQID(9)
E 342	'n' position not defined found at POS: 3 SEQID(9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 342	'n' position not defined found at POS: 1 SEQID(11)
E 342	'n' position not defined found at POS: 2 SEQID(11)
E 342	'n' position not defined found at POS: 3 SEQID(11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

<110> Consortium fuer elektrochemische Industrie GmbH

<120> Feedback-resistant Homoserine-Transsuccinylases

<130> CO-P#######

<140>   10530843
<141>   2007-06-19

<150>
<151>

<160> 12

<170> PatentIn Ver. 2.0

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<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(930)

<300>
<301> Blattner, F. R.
<302> The complete genome sequence of Escherichia coli K-12.
<303> Science
<304> 277
<305> 5331
<306> 1453-1474
<307> 1997

<400> 1
atg ccg att cgt gtg ccg gac gag cta ccc gcc gtc aat ttc ttg cgt   48
Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
 1   5   10   15

gaa gaa aac gtc ttt gtg atg aca act tct cgt gcg tct ggt cag gaa   96
Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
            20   25   30

att cgt cca ctt aag gtt ctg atc ctt aac ctg atg ccg aag aag att   144
Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
        35   40   45

gaa act gaa aat cag ttt ctg cgc ctg ctt tca aac tca cct ttg cag   192
Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
    50   55   60

gtc gat att cag ctg ttg cgc atc gat tcc cgt gaa tcg cgc aac acg   240
Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
 65   70   75   80

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ccc gca gag cat ctg aac aac ttc tac tgt aac ttt gaa gat att cag      288
Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
            85                      90                      95

gat cag aac ttt gac ggt ttg att gta act ggt gcg ccg ctg ggc ctg      336
Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
            100                     105                     110

gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg      384
Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
            115                     120                     125

gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg      432
Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
            130                     135                     140

gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc      480
Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
145                     150                     155                     160

acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat      528
Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
                    165                     170                     175

gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg      576
Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
            180                     185                     190

cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg      624
Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
            195                     200                     205

gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt      672
Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
        210                     215                     220

aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg      720
Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
225                     230                     235                     240

caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac      768
Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
            245                     250                     255

ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca      816
Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
            260                     265                     270

ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg      864
Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
            275                     280                     285

ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg      912
Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
        290                     295                     300

aat cca acg ctg gat taa                                               930
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Asn Pro Thr Leu Asp
305

<210> 2
<211> 309
<212> PRT
<213> Escherichia coli

<400> 2
Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
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Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
             20   25   30

Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
         35   40   45

Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
     50   55   60

Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
 65   70   75   80

Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
                 85   90   95

Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
             100   105   110

Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
         115   120   125

Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
     130   135   140

Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
145   150   155   160

Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
                 165   170   175

Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
             180   185   190

Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
         195   200   205

Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
     210   215   220

Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
225   230   235   240

Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
                 245   250   255

Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
          260   265   270

Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
          275   280   285

Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
     290   295   300

Asn Pro Thr Leu Asp
305

<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
     Oligonucleotide   metAfw

<400> 3
gatcccatgg ctcctttttag tcattcttat   30

<210> 4
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide
     metArev

<400> 4
gatcgagctc agtactatta atccagcgtt ggattc   36

<210> 5
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

     GAPDHfw

<400> 5
gtcgacgcgt gaggcgagtc agtcgcgtaa tgc   33

<210> 6
<211> 42   n=1:1:1:1 mixture of A,T,C and G.

<212> DNA